

受付番号は、【20090106184136_3410】です。

***** [align] *****

options = -align -gapdist=8 -maxdiv=40

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQIDNO_1 881 bp

Sequence 2: B0671560 889 bp

Sequence 3: B0672221 979 bp

Sequence 4: B1914593 735 bp

Start of Pairwise alignments

Aligning...

== Aligned score is not displayed ==

Start of Multiple Alignment

There are 3 groups

Aligning...

== Aligned score is not displayed ==

Alignment Score 33195

query.aln

CLUSTAL W (1.83) multiple sequence alignment

```
SEQIDNO_1      -----GGGCCATGACCCCGCTGCTGTGCTTGCAAGCTCGTC
B1914593
B0672221      CGCGGCTGCCCGAGCGCCGCGCGGCCATGACCCCGCTGCTGTGCTTGCAAGCTCGTC
B0671560      CGCGGCTGCCCGAGCGCCGCGCGGCCATGACCCCGCTGCTGTGCTTGCAAGCTCGTC
```

```
SEQIDNO_1      GCGCGGCCCCCGAGCCCGACCGCCGCCACACCAGCGCCGCGGCGGCTCG
B1914593
B0672221      GCGCGGCCCCCGAGCCCGACCGCCGCCGCCACACCAGCGCCGCGGCGGCTCG
B0671560      GCGCGGCCCCCGAGCCCGACCGCCGCCGCCACACCAGCGCCGCGGCGGCTCG
```

```
SEQIDNO_1      CGCGCCTCGGGCGCGGCTCCGAGTGAGCCACCAAGAAGGAAGCGGCTGCAGAGGTGC
B1914593      -----GCAGTGAGCCACCAAGAAGGAAGCGGCTGCAGAGGTGC
B0672221      CGCGCCTCGGGCGCGGCTCCGAGTGAGCCACCAAGAAGGAAGCGGCTGCAGAGGTGC
B0671560      CGCGCCTCGGGCGCGGCTCCGAGTGAGCCACCAAGAAGGAAGCGGCTGCAGAGGTGC
```

```
SEQIDNO_1      CGACATGGGGCTTAAGATGTCCTGCCTGAAAGGCTTTCAAATGTGTGCAGCAGCAGCAG
B1914593      CGACATGGGGCTTAAGATGTCCTGCCTGAAATGC-----AGCAG
B0672221      CGACATGGGGCTTAAGATGTCCTGCCTGAAAGGCTTTCAAATGTGTGCAGCAGCAGCAG
B0671560      CGACATGGGGCTTAAGATGTCCTGCCTGAAAGGCTTTCAAATGTGTGCAGCAGCAGCAG
```

***** **

```
SEQIDNO_1      CAGCAGCCACGACGAGGCCCGCTGCTGAACGACAAGCACCTGGACGTGCCGACATCAT
B1914593      CAGCAGCCACGACGAGGCCCGCTGCTGAACGACAAGCACCTGGACGTGCCGACATCAT
B0672221      CAGCAGCCACGACGAGGCCCGCTGCTGAACGACAAGCACCTGGACGTGCCGACATCAT
```

B0671560 CAGCAGCCACGACGAGGCCCCCGTCTGTAACGACAAGCACCTGGACGTGCCGACATCAT

SEQIDNO_1 CATCACGCCCCCACCACCACGGGCATGATGCTGCCGAGGGACTTGGGAGCACA GTCTG
B1914593 CATCACGCCCCCACCACCACGGGCATGATGCTGCCGAGGGACTTGGGAGCACA GTCTG
B0672221 CATCACGCCCCCACCACCACGGGCATGATGCTGCCGAGGGACTTGGGAGCACA GTCTG
B0671560 CATCACGCCCCCACCACCACGGGCATGATGCTGCCGAGGGACTTGGGAGCACA GTCTG

SEQIDNO_1 GCTGGATGAGACAGGGTGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGG
B1914593 GCTGGATGAGACAGGGTGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGG
B0672221 GCTGGATGAGACAGGGTGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGG
B0671560 GCTGGATGAGACAGGGTGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGG

SEQIDNO_1 TGTCTG66T1TTGGCTGGCTGGCTCCTGCTCCAGCGGCCGGCTTCAGGTGTCCG66GGC
B1914593 TGTCTG66T1TTGGCTGGCTGGCTCCTGCTCCAGCGGCCGGCTTCAGGTGTCCG66GGC
B0672221 TGTCTG66T1TTGGCTGGCTGGCTCCTGCTCCAGCGGCCGGCTTCAGGTGTCCG66GGC
B0671560 TGTCTG66T1TTGGCTGGCTGGCTCCTGCTCCAGCGGCCGGCTTCAGGTGTCCG66GGC

SEQIDNO_1 GTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACCTGAGCGAACCC-GGGCC
B1914593 GTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACCTGAGCGAACCC-GGGCC
B0672221 GTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACCTGAGCGAACCC-GGGCC
B0671560 GTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACCTGAGCGAACCC-GGGCC

SEQIDNO_1 TCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCAC-TTCAGAACA
B1914593 TCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCAC-TTCAGAACA
B0672221 TCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCAC-TTCAGAACA
B0671560 TCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCAC-TTCAGAACA

SEQIDNO_1 GTGTTTCCAG66CCC-GCTGAGTGGACCG6ACCTGTGACACCTCCAG6TTCTTGCTGAC
B1914593 GTGTTTCCAG66CCC-GCTGAGTGGACCG6ACCTGTGACACCTCCAG6TTCTTGCTGAC
B0672221 GTGTTTCCAG66CCC-GCTGAGTGGACCG6ACCTGTGACACCTCCAG6TTCTTGCTGAC
B0671560 GTGTTTCCAG66CCC-GCTGAGTGGACCG6ACCTGTGACACCTCCAG6TTCTTGCTGAC

SEQIDNO_1 TCCGGCCTGGTGAAGGGAGCGCCATGGTCC-TGGCTGTTGG6GT-CCCAG6GAGAGGT
B1914593 TCCGGCCTGGTGAAGGGAGCGCCATGGTCC-TGGCTGTTGG6GT-CCCAG6GAGAGGT
B0672221 TCCGGCCTGNTGAAGGGAGCGCCATGGTCC-TGGCTGGTGG6GT-CCCAG6GAGAGGT
B0671560 TCCGGCCTGGGGAAGGGAAACGCTTGGTCCCTGGCTGTTGGGGGCCCAAGGAAAGGT

SEQIDNO_1 CTC-TTCTGGACAAACACAGCCTGCCAGCCCG-AGGGCTGTGCA-AACACATGCCCTG
B1914593 CTC-TTCTGGACAAACACAGCCTGCCAGCCCGAGGGCTGTGCA-AACACATGCCCTG
B0672221 CTGCTTCTGGACAAACACACCTTCCAGGCCCGAGGGCTGTGCA-AACACATGCCCTG
B0671560 CGTCTTCCGAGCAAAACGAACCTTTGAAAGCCCCCGGGCATGGACAAACAAAGCCCCG
* * * * *

SEQIDNO_1 ---CCATAAGCAACAAGAAGTCTTT---GCAGGTGGAGTGGCTGTTTTTATAAGTT---
B1914593 ---CCATAAGCAACAAGAAGTCTTT---GCAGGTGGAGTGGCTGTTTTTATAAGTT---
B0672221 G---CCATAAGCCCCCAAAAACCTTCTTGGCCGGGGAGGGGTTTTTTTTTAAAGCC
B0671560 GTCCATGGACCCCGAGGAAGAAGTTCCTTGGAGGCCGGGGGGGAATCGGGCTGTACC-
* * * * *

SEQIDNO_1 ---GTTTTACAGA---TACGGAACAGTCCAAAATGGGA---TTTATAATTTCTTTTTG
B1914593 ---GTTTTACAGA---TACGGAACAGTCCAAAATGGGA---TTTATAATTTCTTTTTG
B0672221 CGCGTTTTACGCAGTGGCGACAACCCCCATACCGGGACTCTATCACTTCTCACTTG
B0671560 -----TACCAAGCTTACAGGACTCGGCGGAAAAGGA-----CGGCGCAAGGGCCG
* * * * *

```

SEQIDNO_1      CATTATAATAA-----AGATCCTGTGAAC-----
B1914593      CATTATAATAA-----AGATCC-----
B0672221      CGCCATGATCGAGGCGAGGTCTTTCGTGCCCCGCCGACACAGGCTCGGCCCCGT
B0671560      CGCCGG-----
*
```

```

SEQIDNO_1      -----
B1914593      -----
B0672221      ACCATCCGCGGATCGCCGGGCACCG
B0671560      -----
```

```

query.dnd
(
  SEQIDNO_1:-0.00673,
  (
    B0671560:0.09278,
    B0672221:0.04332)
  :0.06807,
  B1914593:0.01353);
```

***** [tree] *****

options = -tree -kimura -tossgaps

CLUSTAL W (1.83) Multiple Sequence Alignments

```

Sequence format is Clustal
Sequence 1: SEQIDNO_1      985 bp
Sequence 2: B1914593      985 bp
Sequence 3: B0672221      985 bp
Sequence 4: B0671560      985 bp
```

```

query.ph
(
  SEQIDNO_1:-0.00039,
  B1914593:0.00602)
:0.03370,
  B0672221:0.02953,
  B0671560:0.11040);
```